Please amend the following claims:

Claim 2 (Twice Amended), line 2, please change "1" to --13--.

Claim 3 (Thrice Amended), line 2, please change "1" to --13--.

Claim 4 (Amended) A nucleic acid assay process according to claim [1] 13, wherein the analyte nucleic acid is selected from the group consisting of:

a cancer-related gene, a gene related to genetic disease, a virus gene, a bacteria gene, [or] and a polymorphic host gene.

Claim 5 (Amended) A nucleic acid assay process according to claim [1] 13, wherein the analyte nucleic acid is selected from the group consisting of:

k-ras gene, N-ras gene, p53 gene, BRCA1 gene, BRCA2 gene, [or] and APC gene [which is a cancer-related gene].

Claim 6 (Twice Amended), line 1, please change "1" to --13--.

Claim 7 (Twice Amended), line 1, please change "1" to --13--.

Claim 8 (Twice Amended), line 1, please change "1" to --13--.

Claim 9 (Twice Amended), line 2, please change "1" to --13--.

Claim 12 (Amended), line 1, please change "11" to --13--.

Please add the following claim:

--13. A nucleic acid assay process for identifying and/or quantifying a mutation or polymorphism in a sample DNA comprising the steps of:

providing a labeled standard DNA having a nucleotide sequence the same as a mutated or polymorphic target DNA of interest, wherein said labeled standard DNA comprises a double stranded nucleic acid having a site capable of binding to a solid support on one strand and a detectable label on the other strand;

amplifying a particular region of an analyte nucleic acid in a specimen to prepare a double stranded sample DNA, wherein said sample DNA comprises both wild-type and mutated or polymorphic target DNA;

selecting a detection limit for said mutated or polymorphic target DNA, wherein when the detection limit for the target DNA present in said sample DNA is A/B, the excessiveness of said sample DNA is at least B/A, and wherein A/B is the fractional equivalent of the percentage of target DNA content in the sample DNA;

adding an excessive amount of said sample DNA to said labeled standard DNA, to allow competitive hybridization to take place, wherein the excessiveness of said sample DNA added to said labeled standard DNA in the competitive hybridization is selected in accordance with the pre-selected detection limit,

detecting the rehybridized labeled standard DNA by utilizing said detectable label and said site capable of binding to a solid support; and

evaluating the degree of exchange of the complementary strands between said sample DNA and said labeled standard DNA.--

REMARKS

The Office Action of April 27, 2000 presents the examination of claims 1-12. Claims 1 and 11 are canceled herein. Claims 2-9, and 12 are amended. Claim 13 is added for consideration of the Examiner. Support for claim 13 is found in the specification, especially page 19, lines 14-20, and in the